

CHANGES MADE." Applicants note that those claims not amended herein are being reiterated solely for the convenience of the Examiner.

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AMENDMENTS**IN THE FIGURES**

Please replace Figures 1 and 4-8 with the amended Figures 1, 4, 5A-5D, 6A-6D, 7A-7D, and 8A-8D as indicated in the Request for Approval of Proposed Drawing Amendment submitted herewith.

IN THE SPECIFICATION:

Delete pages 20-28 of the specification (the Sequence Listing).

Renumber pages 29-33 as pages 20-24.

Insert new page 25 entitled "Abstract of the Invention" after newly renumbered page 24 (after the claims).

Insert the enclosed document entitled "Sequence Listing", numbered beginning with page 1 after the abstract.

Replace the paragraph bridging pages 7-8 with the following:

FIG. 1A Human VDR gene locus. Four overlapping cosmid clones were isolated from a human lymphocyte genomic library (Stratagene) and directly sequenced. Clone J5 extends from the 5' flanking region to intron 2; AE, from intron 1b to intron 5; D2, from intron 3 to the 3' UTR; WE, from intron 6 through the 3' flanking region. Sequence upstream of exon 1f was obtained by anchored PCR from genomic DNA. **FIG. 1B** Structure of hVDR transcripts.

Transcripts 1-5 originate from exon 1a. Transcript 1 corresponds to the published cDNA (1). Transcripts 6-10 originate from exon 1d and transcripts 11-14 originate from exon 1f. Boxed numbers indicate the major transcript (based on the relative intensities of the multiple PCR products) within each exon-specific group of transcripts generated with a single primer set.

While all transcripts have a translation initiation codon in exon 2, exon 1d transcripts have the potential to initiate translation upstream in exon 1d, with transcripts 6 and 9 encoding VDR proteins with extended N termini. **FIG. 1C** N-terminal variant proteins encoded by novel hVDR transcripts. Transcript 1 corresponds to the published cDNA sequence (1) and encodes the 427-aa hVDR protein. Transcripts 6 and 9 code for a protein with an extra 50 aa or 23 aa, respectively, at the N-terminal. The 23 aa of the hVDR A/B domain are shown in bold.

Replace the paragraphs at page 9 lines 17 to 35 with the following:

FIGS. 5A-5D. Provides the nucleotide sequence corresponding to transcript 6 (see figure 1) (SEQ ID NO: 2), together with the predicted amino acid sequence (SEQ ID NO: 9) of the encoded protein. Nucleotides 1-96 correspond to exon 1d; nucleotides 97-1463 correspond to exons 1c to the stop codon in exon 9 (or nucleotides -83-1283 of the hVDR cDNA (1)).

FIGS. 6A-6D. Provides the nucleotide sequence corresponding to transcript 9 (see figure 1) (SEQ ID NO: 3), together with the predicted amino acid sequence (SEQ ID NO: 10) of the encoded protein. Nucleotides 1-96 correspond to exon 1d; nucleotides 97 - 1382 correspond to exon 2 to the stop codon in exon 9 (or nucleotides -2 - 1283 of the hVDR cDNA (1)).

FIGS. 7A-7D. Provides the nucleotide sequence corresponding to transcript 10 (see figure 1) (SEQ ID NO: 4), together with the predicted amino acid sequence (SEQ ID NO: 11) of the encoded protein. Nucleotides 1-96 correspond to exon 1d; nucleotides 97-244 correspond to exon 2; nucleotides 245-396 correspond to intronic sequence immediately 3' to exon 2; nucleotides 397-1534 correspond to exons 3 to the stop codon in exon 9 (or nucleotides 146-1283 of the hVDR cDNA (1)).

Replace the paragraph beginning at page 10, line 1 with the following:

FIGS. 8A-8D. Provides the nucleotide sequence corresponding to transcript 11 (see figure 1) (SEQ ID NO: 7), together with the predicted amino acid sequence (SEQ ID NO: 12) of the encoded protein. Nucleotides 1-207 correspond to exon 1f; nucleotides 208-1574 correspond to exon 1c to the stop codon in exon 9 (or nucleotides -83-1283 of the hVDR cDNA (1)).

IN THE CLAIMS

Replace the claims with the clean copy of their correspondingly numbered claims below.

Add new claims 26-29.

1. (**Amended**) An isolated polynucleotide molecule encoding a human vitamin D receptor (hVDR) isoform, said polynucleotide molecule comprising i) a nucleotide sequence having 95% or more